Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (Previously presented) A method of diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease, said method comprising:

(a) genotyping an individual for the presence or absence of the SNP 13 allele in the NOD2/CARD15 gene using enzymatic amplification of nucleic acid from said individual, wherein said SNP 13 allele is an insertion of a G at position 248 of SEQ ID NO:5 or an insertion of a C at position 294 of SEQ ID NO:6; and

(b) indicating that the presence of said SNP 13 allele is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease.

2. (Canceled)

3. (Canceled)

4. (Previously presented) The method of claim **1**, wherein NF-kappa B activation by a NOD2/CARD15 polypeptide encoded by said SNP 13 allele is reduced as compared to NF-kappa B activation by a wild-type NOD2/CARD15 polypeptide.

5-15. (Canceled)

16. (Previously presented) The method of claim **1**, wherein said SNP 13 allele is associated with said clinical subtype of Crohn's disease characterized by fibrostenosing disease with an odds ratio of at least 2 and a lower 95% confidence limit greater than 1.

17. (Previously presented) The method of claim **1**, further comprising generating a report indicating the presence or absence in said individual of said SNP 13 allele.

18. (Previously presented) The method of claim **1**, further comprising generating a report indicating the presence or absence in said individual of said clinical subtype of Crohn's disease characterized by fibrostenosing disease.

19. (Canceled)

20. (Previously presented) The method of claim **1**, wherein said amplification is polymerase chain reaction amplification.

21. (Original) The method of claim **20**, wherein said polymerase chain reaction amplification is performed using one or more fluorescently labeled probes.

22. (Previously presented) The method of claim **20**, wherein said polymerase chain reaction amplification is performed using one or more probes comprising a DNA minor groove binder.

23. (Previously presented) A method of optimizing therapy in an individual, said method comprising:

(a) genotyping an individual for the presence or absence of the SNP 13 allele in the NOD2/CARD15 gene using enzymatic amplification of nucleic acid from said individual, wherein said SNP 13 allele is an insertion of a G at position 248 of SEQ ID NO:5 or an insertion of a C at position 294 of SEQ ID NO:6;

(b) diagnosing individuals in which said SNP 13 allele is present as having a fibrostenosing subtype of Crohn's disease; and

(c) treating said individual having a fibrostenosing subtype of Crohn's disease based on said diagnosis.

24. (Previously presented) The method of claim **23**, wherein said SNP 13 allele is associated with said clinical subtype of Crohn's disease characterized by fibrostenosing disease with an odds ratio of at least 2 and a lower 95% confidence limit greater than 1.

25. (Previously presented) The method of claim **23**, further comprising generating a report indicating the presence or absence in said individual of said SNP 13 allele.

26. (Previously presented) The method of claim **23**, further comprising generating a report indicating the presence or absence in said individual of said clinical subtype of Crohn's disease characterized by fibrostenosing disease.

27. (Canceled)

28. (Previously presented) The method of claim **23**, wherein said amplification is polymerase chain reaction amplification.

29. (Previously presented) The method of claim **28**, wherein said polymerase chain reaction amplification is performed using one or more fluorescently labeled probes.

30. (Previously presented) The method of claim **28**, wherein said polymerase chain reaction amplification is performed using one or more probes comprising a DNA minor groove binder.